RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____10/578,939_____

Source: _____IFWP_____

Date Processed by STIC: _____05/19/2006_____

ENTERED

IFWP

RAW SEQUENCE LISTING   DATE: 05/19/2006
PATENT APPLICATION: US/10/578,939   TIME: 08:39:24

Input Set : F:\210850067SEQLIST.TXT
Output Set: N:\CRF4\05192006\J578939.raw

```
  4 <110> APPLICANT: UAB Research Foundation
  5        van Ginkel, Frederik W.
  6        Briles, David E.
  7        Watt, James M.
 10 <120> TITLE OF INVENTION: COMPOSITION FOR REDUCING BACTERIAL
 11        CARRIAGE AND CNS INVASION AND METHODS OF USING SAME
 14 <130> FILE REFERENCE: 21085.0067P1
```
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/578,939
C--> 16 <141> CURRENT FILING DATE: 2006-05-09
```
 16 <150> PRIOR APPLICATION NUMBER: 60/518,799
 17 <151> PRIOR FILING DATE: 2003-11-10
 19 <160> NUMBER OF SEQ ID NOS: 17
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 23
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
 30        Synthetic Construct
 32 <400> SEQUENCE: 1
 33 atttctgtaa cagctaccaa cga                                      23
 35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 23
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Artificial Sequence
 40 <220> FEATURE:
 41 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
 42        Synthetic Construct
 44 <400> SEQUENCE: 2
 45 gaattccctg tcttttcaaa gtc                                      23
 47 <210> SEQ ID NO: 3
 48 <211> LENGTH: 20
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Artificial Sequence
 52 <220> FEATURE:
 53 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
 54        Synthetic Construct
 56 <400> SEQUENCE: 3
 57 ccgatacact ctcttcccga                                         20
 59 <210> SEQ ID NO: 4
 60 <211> LENGTH: 20
 61 <212> TYPE: DNA
```

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```
 62 <213> ORGANISM: Artificial Sequence
 64 <220> FEATURE:
 65 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
 66      Synthetic Construct
 68 <400> SEQUENCE: 4
 69 acagttggtg ctaaggaggc                                              20
 71 <210> SEQ ID NO: 5
 72 <211> LENGTH: 15
 73 <212> TYPE: PRT
 74 <213> ORGANISM: Artificial Sequence
 76 <220> FEATURE:
 77 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
 78      Synthetic Construct
 80 <400> SEQUENCE: 5
 81 Val Trp Arg Leu Leu Ala Pro Pro Phe Ser Asn Arg Leu Leu Pro
 82  1               5                   10                  15
 84 <210> SEQ ID NO: 6
 85 <211> LENGTH: 34
 86 <212> TYPE: DNA
 87 <213> ORGANISM: Artificial Sequence
 89 <220> FEATURE:
 90 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
 91      Synthetic Construct
 93 <400> SEQUENCE: 6
 94 cgcggatcct catactgggt taggaaagtc gtcg                              34
 96 <210> SEQ ID NO: 7
 97 <211> LENGTH: 37
 98 <212> TYPE: DNA
 99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
103      Synthetic Construct
105 <400> SEQUENCE: 7
106 ggaattccat atgccgacag cagaactacc taaaggc                           37
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 41
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial Sequence
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
115      Synthetic Construct
117 <400> SEQUENCE: 8
118 ggaattccat atgctggcaa atgaaactca actttcgggg g                      41
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 29
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
```

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```
127        Synthetic Construct
129 <400> SEQUENCE: 9
130 cgcggatcca tcggctttga ccatcggag                              29
132 <210> SEQ ID NO: 10
133 <211> LENGTH: 38
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
139        Synthetic Construct
141 <400> SEQUENCE: 10
142 ggaattccat atgcgtattc cagcacttct caagacag                    38
144 <210> SEQ ID NO: 11
145 <211> LENGTH: 21
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
151        Synthetic Construct
153 <400> SEQUENCE: 11
154 ggaacattac ctcgcaaaag g                                      21
156 <210> SEQ ID NO: 12
157 <211> LENGTH: 19
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
163        Synthetic Construct
165 <400> SEQUENCE: 12
166 tacccgcagg cataacatc                                         19
168 <210> SEQ ID NO: 13
169 <211> LENGTH: 5
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
175        Synthetic Construct
177 <400> SEQUENCE: 13
178 Leu Pro Glu Thr Gly
179  1                 5
181 <210> SEQ ID NO: 14
182 <211> LENGTH: 5
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =
188        Synthetic Construct
W--> 190 <221> NAME/KEY: VARIANT
191 <222> LOCATION: 3
```

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```
    192 <223> OTHER INFORMATION: Xaa = any amino acid.
W--> 194 <400> 14
W--> 195 Leu Pro Xaa Thr Gly
    196 1                5
    198 <210> SEQ ID NO: 15
    199 <211> LENGTH: 1035
    200 <212> TYPE: PRT
    201 <213> ORGANISM: S. pneumoniae
    203 <400> SEQUENCE: 15
    204 Met Ser Tyr Phe Arg Asn Arg Asp Ile Asp Ile Glu Arg Asn Ser Met
    205 1               5                   10                  15
    206 Asn Arg Ser Val Gln Glu Arg Lys Cys Arg Tyr Ser Ile Arg Lys Leu
    207             20                  25                  30
    208 Ser Val Gly Ala Val Ser Met Ile Val Gly Ala Val Val Phe Gly Thr
    209             35                  40                  45
    210 Ser Pro Val Leu Ala Gln Glu Gly Ala Ser Glu Gln Pro Leu Ala Asn
    211     50                  55                  60
    212 Glu Thr Gln Leu Ser Gly Glu Ser Ser Thr Leu Thr Asp Thr Glu Lys
    213 65                  70                  75                  80
    214 Ser Gln Pro Ser Ser Glu Thr Glu Leu Ser Gly Asn Lys Gln Glu Gln
    215             85                  90                  95
    216 Glu Arg Lys Asp Lys Gln Glu Glu Lys Ile Pro Arg Asp Tyr Tyr Ala
    217             100                 105                 110
    218 Arg Asp Leu Glu Asn Val Glu Thr Val Ile Glu Lys Glu Asp Val Glu
    219             115                 120                 125
    220 Thr Asn Ala Ser Asn Gly Gln Arg Val Asp Leu Ser Ser Glu Leu Asp
    221     130                 135                 140
    222 Lys Leu Lys Lys Leu Glu Asn Ala Thr Val His Met Glu Phe Lys Pro
    223 145                 150                 155                 160
    224 Asp Ala Lys Ala Pro Ala Phe Tyr Asn Leu Phe Ser Val Ser Ser Ala
    225             165                 170                 175
    226 Thr Lys Lys Asp Glu Tyr Phe Thr Met Ala Val Tyr Asn Asn Thr Ala
    227             180                 185                 190
    228 Thr Leu Glu Gly Arg Gly Ser Asp Gly Lys Gln Phe Tyr Asn Asn Tyr
    229         195                 200                 205
    230 Asn Asp Ala Pro Leu Lys Val Lys Pro Gly Gln Trp Asn Ser Val Thr
    231     210                 215                 220
    232 Phe Thr Val Glu Lys Pro Thr Ala Glu Leu Pro Lys Gly Arg Val Arg
    233 225                 230                 235                 240
    234 Leu Tyr Val Asn Gly Val Leu Ser Arg Thr Ser Leu Arg Ser Gly Asn
    235             245                 250                 255
    236 Phe Ile Lys Asp Met Pro Asp Val Thr His Val Gln Ile Gly Ala Thr
    237             260                 265                 270
    238 Lys Arg Ala Asn Asn Thr Val Trp Gly Ser Asn Leu Gln Ile Arg Asn
    239         275                 280                 285
    240 Leu Thr Val Tyr Asn Arg Ala Leu Thr Pro Glu Glu Val Gln Lys Arg
    241     290                 295                 300
    242 Ser Gln Leu Phe Lys Arg Ser Asp Leu Glu Lys Lys Leu Pro Glu Gly
    243 305                 310                 315                 320
```

```
244 Ala Ala Leu Thr Glu Lys Thr Asp Ile Phe Glu Ser Gly Arg Asn Gly
245             325             330             335
246 Lys Pro Asn Lys Asp Gly Ile Lys Ser Tyr Arg Ile Pro Ala Leu Leu
247             340             345             350
248 Lys Thr Asp Lys Gly Thr Leu Ile Ala Gly Ala Asp Glu Arg Arg Leu
249         355             360             365
250 His Ser Ser Asp Trp Gly Asp Ile Gly Met Val Ile Arg Arg Ser Glu
251     370             375             380
252 Asp Asn Gly Lys Thr Trp Gly Asp Arg Val Thr Ile Thr Asn Leu Arg
253 385             390             395             400
254 Asp Asn Pro Lys Ala Ser Asp Pro Ser Ile Gly Ser Pro Val Asn Ile
255             405             410             415
256 Asp Met Val Leu Val Gln Asp Pro Glu Thr Lys Arg Ile Phe Ser Ile
257             420             425             430
258 Tyr Asp Met Phe Pro Glu Gly Lys Gly Ile Phe Gly Met Ser Ser Gln
259         435             440             445
260 Lys Glu Glu Ala Tyr Lys Lys Ile Asp Gly Lys Thr Tyr Gln Ile Leu
261     450             455             460
262 Tyr Arg Glu Gly Glu Lys Gly Ala Tyr Thr Ile Arg Glu Asn Gly Thr
263 465             470             475             480
264 Val Tyr Thr Pro Asp Gly Lys Ala Thr Asp Tyr Arg Val Val Val Asp
265             485             490             495
266 Pro Val Lys Pro Ala Tyr Ser Asp Lys Gly Asp Leu Tyr Lys Gly Asn
267             500             505             510
268 Gln Leu Leu Gly Asn Ile Tyr Phe Thr Thr Asn Lys Thr Ser Pro Phe
269         515             520             525
270 Arg Ile Ala Lys Asp Ser Tyr Leu Trp Met Ser Tyr Ser Asp Asp Asp
271     530             535             540
272 Gly Lys Thr Trp Ser Ala Pro Gln Asp Ile Thr Pro Met Val Lys Ala
273 545             550             555             560
274 Asp Trp Met Lys Phe Leu Gly Val Gly Pro Gly Thr Gly Ile Val Leu
275             565             570             575
276 Arg Asn Gly Pro His Lys Gly Arg Ile Leu Ile Pro Val Tyr Thr Thr
277             580             585             590
278 Asn Asn Val Ser His Leu Asn Gly Ser Gln Ser Ser Arg Ile Ile Tyr
279             595             600             605
280 Ser Asp Asp His Gly Lys Thr Trp His Ala Gly Glu Ala Val Asn Asp
281     610             615             620
282 Asn Arg Gln Val Asp Gly Gln Lys Ile His Ser Ser Thr Met Asn Asn
283 625             630             635             640
284 Arg Arg Ala Gln Asn Thr Glu Ser Thr Val Val Gln Leu Asn Asn Gly
285             645             650             655
286 Asp Val Lys Leu Phe Met Arg Gly Leu Thr Gly Asp Leu Gln Val Ala
287             660             665             670
288 Thr Ser Lys Asp Gly Gly Val Thr Trp Glu Lys Asp Ile Lys Arg Tyr
289         675             680             685
290 Pro Gln Val Lys Asp Val Tyr Val Gln Met Ser Ala Ile His Thr Met
291     690             695             700
292 His Glu Gly Lys Glu Tyr Ile Ile Leu Ser Asn Ala Gly Gly Pro Lys
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/19/2006
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 3

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:16; Line(s) 461

VERIFICATION SUMMARY   DATE: 05/19/2006
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L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:190 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:194 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0